Mutant-specific oligonucleotide primers used for mutant number 1. Mutated nucleotide underlined.

Bet v 1 sense	5'- A	ATTATGAGACTGAGACC <u>A</u> CCTCTGTTATCCCAGCAGCTCG	-3 '
Bet v 1 non-sense	3'- T	TAATACTCTGACTCTGG <u>T</u> GGAGACAATAGGGTCGTCGAGC	<b>-5</b> '
sense primer	5'-	TGAGACC <u>C</u> CCTCTGTTATCCCAG	-3 '
non-sense primer	3 ' -	ATACTCTGACTCTGG <u>G</u> GGAGAÇA	-51

Oligonucleotide primers for site directed mutagenesis of Bet v 1 (No. 2801).

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4:186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 1878v, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTCAGGAAATGGAGGGCC
3	non-sense	7: 1898v, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 1918v, 23-mer 5'-AGCIGATGTTCTTAATGGTTCCA
5	sense	10: 1928v, 23-mer 5'-GGACCATGCAAACTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

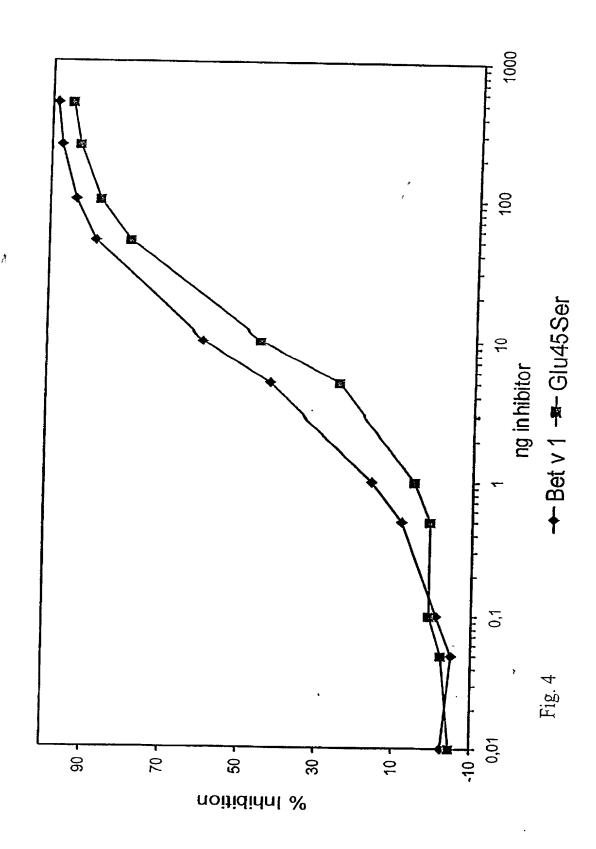
# Overview of all Bet v 1 mutations

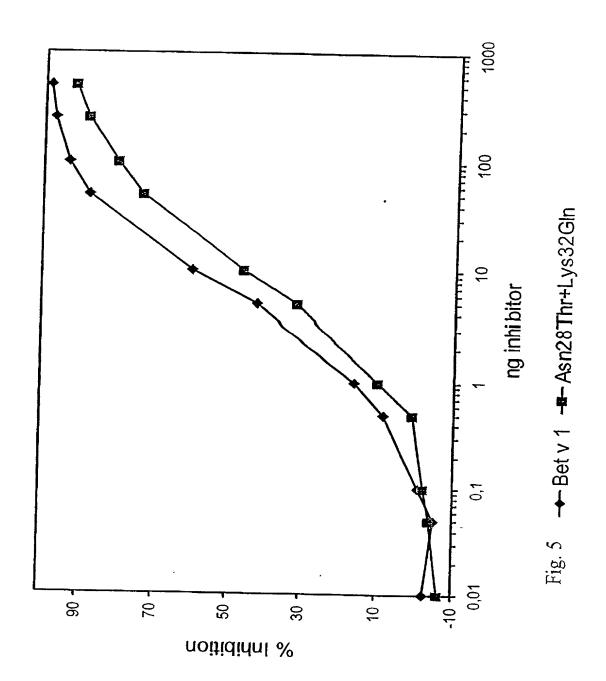
									1 (	A-C	:}									
GG?	rgt(	TT.	AA1	TTA.	rga	GAC	TGA	GAC	CAC	CTC	TGT	TAT	ccc	AGC	4GC	TCGI	CI	HT	CAAG	60
G	v	F	N	Y	Е	T	E	T	<b>T</b> -	PS	v	I	Þ	A	A	R	L	F	ĸ	20
	9 (A-G) 2 (A-C) 2 (A-C)																			
GCC	TT	YTA'	CT	rg <u>a</u> n	GG	CGA	TA <u>A</u> C	CI	CTT:	rcc	A <u>A</u> AG	GTI	GC	ACCC	CA.	AGCC	ATT	AG	ZAGT	120
А	F	I	L	D-G	G	D	N-7	r Ł	F	₽	ĸ-Q	V	A	P	Q	A	I	s	s	40
3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)																				
GTT	GAA	AAC	AT	r <u>ga</u> a	GGF	VAΑ'	rgga	GGG	3CC1	rgg/	AACC	ATT	AAC	BAA <u>G</u>	AT	CAGC	TTT	ccc	<u>ga</u> a	180
v	E	N	I	E-S	G	N-8	S G	G	₽	G	T	1	K	K-N	I	s	F	₽	E-S	60
															5	(CA	-TG	)		
GGC	CTC	CCT	TTC	CAAG	TAC	GT	BAAG	GAC	AGA	GTI	TAD	GAG	GTG	GAC	CAC	<u>'A</u> CA	AAC	TTC	AAA	240
G	Ł	₽	F	ĸ	Y	v	ĸ	D	R	v	D	E	v	D	H	T-A	N	F	ĸ	80
TAC	AAT	rac.	AGC	GTG	ATC	GAC	GGC	GGI	ccc	ATA	GGC	BAC	ACA	TTG	3AG	AAG	ATC	rcc	AAC	300
Y	N	Y	s	V	I	£	G	G	P	I	G	D	T	L	E	ĸ	r	s	N	100
10 (	GAG	-CA	C)		8	(CC	C-T	GG)												
GAG	ATA	AAG.	ATA	GTG	GCA	AC <u>C</u>	CCT	GAT	GGA	GGA	TCC	\TC	TTG	AAG	<b>ATC</b>	'AGC	AAC	AAG	TAC	360
E	I	ĸ	1	v	A	т	P-G	D	.G	G	s	r	L	ĸ	r	s	N	ĸ	Y	120
CACACCAAAGGTGACCATGAGGTGAAGGCAGGCAGGTTAAGGCAAGTAAAGAAATGGGC							420													
н	T	ĸ	G	D	н	E	v	к	A	E	Q	v	ĸ	A	s	ĸ	E	м	G	140

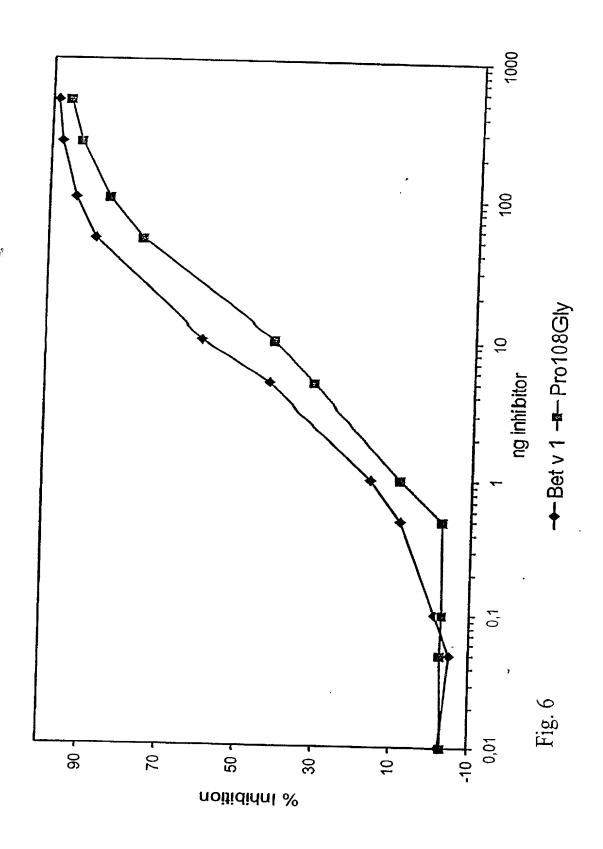
 ${\tt GAGACACTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAACTAA}$ 

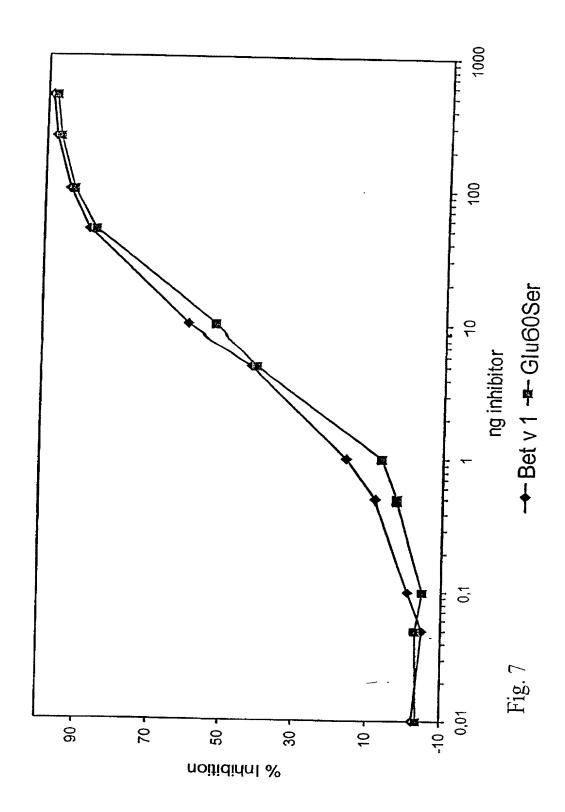
E T L L R A V E S Y L L A H S D A Y N stop

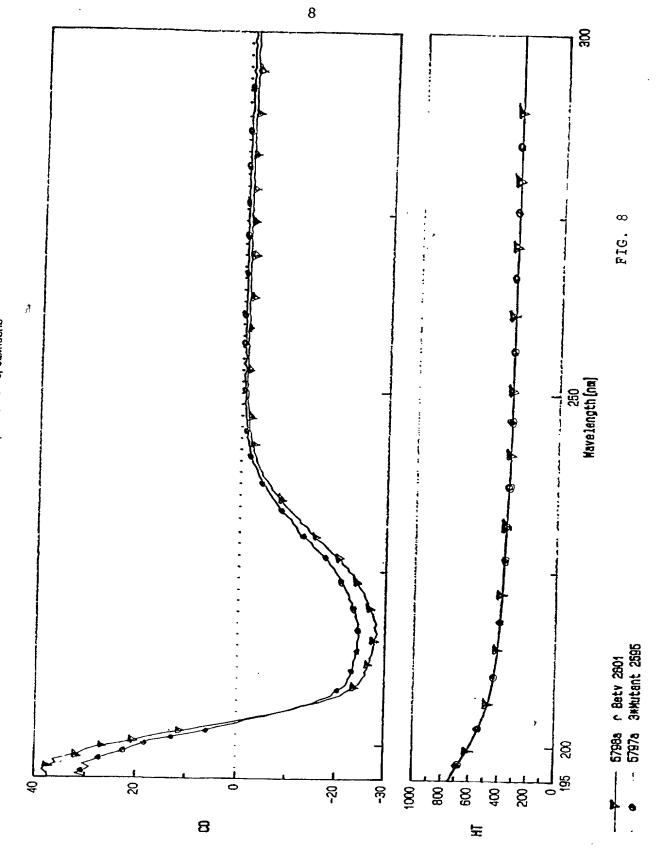
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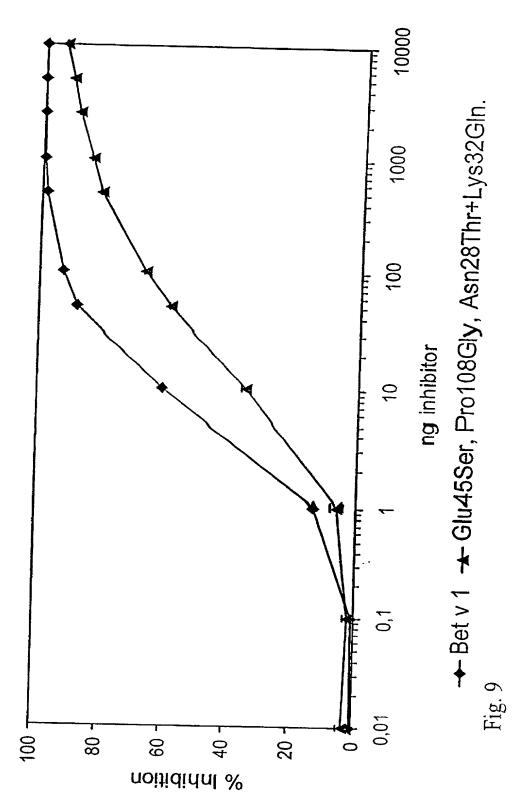












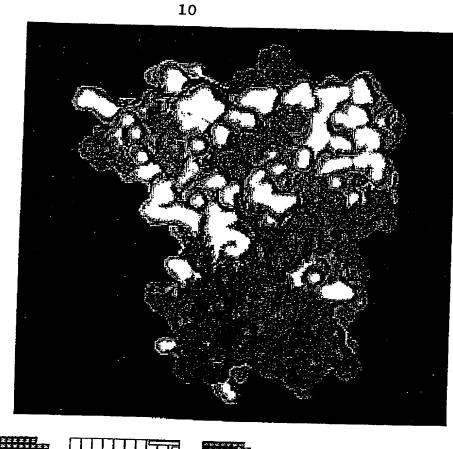
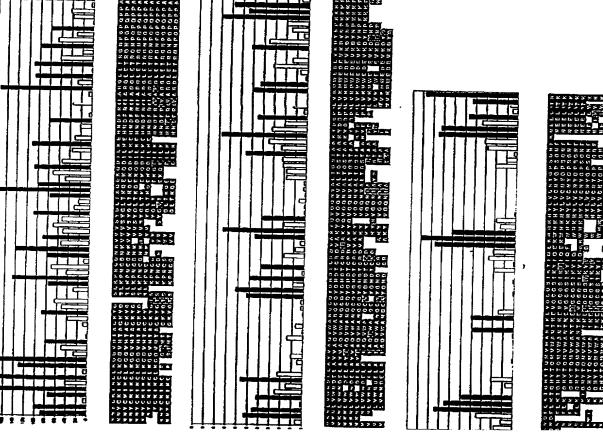


Figure 10.



Mutant-specific oligonucleotide primers used for Ves v 5 mutants. Mutated nucleotides underlined.

#### Ves v 5 mutant 1 (K72A) Ves v 5 sense 5 - ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA -3 -Ves v 5 non-sense 3 - TGGTGTCGGAGGTCGCTTCTTATACTTTTTAAACCATACCT -5 ' sense primer 5 -CCAGCGGCTAATATGAAAAAT -31 non-sense primer 3'-**GTCGGAGGTCGCCGATTATAC** ~5^ Ves v 5 mutant 2 (Y96A) Ves v 5 sense 5 - GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG -3 -Ves v 5 non-sense 3 - CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC -5 1 sense primer 5 ~ TGTCAAGCTGGTCACGATACT -3~ non-sense primer 3 ~ TTAGTTACAGTT<u>CG</u>ACCAGTG -51

Oligonucleotide primers for site directed mutagenesis of Ves v 5.

all sense 1: XhoI start, 38-mer:

#### Ecori

5 -CCGCTCGAGAAAGAAACAATTATTGTAAAATAAATG

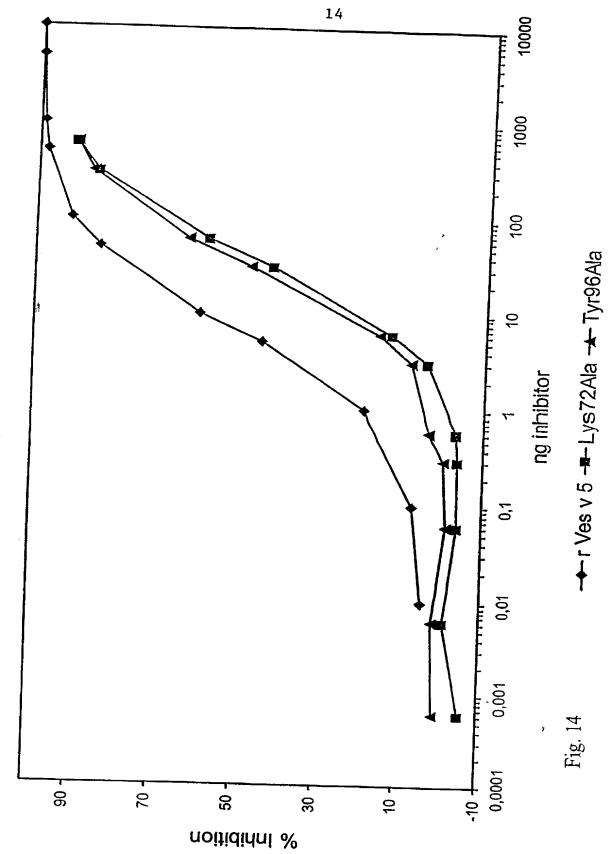
L E K R N N Y C K I K .

Kex2 cleavage site amino terminus of Ves v 5

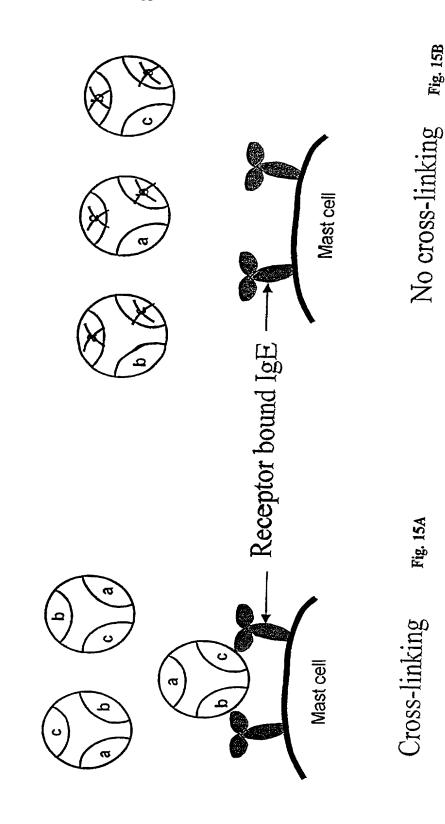
1 sense	1: K72As 21-mer	5~-CCAGCGGCTAATATGAAAAAT
1 non-sense	2: K72Aa 21-mer	5~-CATATTAGCCGCTGGAGGCTG
2 sense	3: Y96As 21-mer	5 1-TGTCAAGCTGGTCACGATACT
2 non-sense	4: Y96Aa 21-mer	5 - GTGACCAGCTTGACATTGATT
2 non-sense	4: 190Ad 21-MC1	3 -GIGACCAGCIIGACAIIGAII
Å		
all non-sense	7: CT-pPICZαA, 21-mei	5 - ATTCATCAGCTGCGAGATAGG
art non bence	i. or pricount, er mer	. J milandidendentind

# Overview of Ves v 5 mutations

1	AA	CAAC	TA:	ľŒ	TAA	AAT.	AAA	ATG'	TTT	GAA	AGG.	AGG'	rgt(	CCA:	rac	TGC	CTG	CAA	ATA:	rgga	6
1	N	N	Y	С	ĸ	Ι	K	С	L	K	G	G	V	H	T	A	С	K	Y	G	20
61	AGT	CTI	1AA1	ACC(	GAA'	rtg	CGG!	raa:	)AAT	GT?	AGT(	GT1	ATC	CTAT	rgg'	гста	AAC	SAAZ	ACA	AGAG	120
21	S	L	K	P	N	C	G	N	K	V	V	V	s	Y	G	L	T	K	Q	E	4
121	AAA	CAA	\GAC	CATO	CTT	LAA(	3GAC	3CA(	CAAC	rgac	TT	raga	\CAI	AAA.	ATT	rgcz	ACG?	AGGI	TTC	GAG	180
41	ĸ	Q	D	I	L	K	E	H	N	D	F	R	Q	K	I	A	R	G	L	E	60
	3 (30	. N. C. K		13. 3.0	naaa	2001	· aa	an c	1000	2001				A] (					mac	** • •	0.46
61	AC1 T												_	M							240 80
																				GC)	
241																				ACT	300
81	D	Е	L	A	Y	V	A	Q	V	W	A	N	Q	С	Q	Y	G	H	D	T	100
301	TGC	AGG	GAT	GTA	.GCA	AAA	TAT	CAG	ĠTT	'GGA	CAA	AAC	:GTA	GCC	TT	ACA	GGT	AGC	ACG	GCT	360
101	C	R	D	v	A	ĸ	Y	Q	v	G	Q	N	v	A	L	т	G	ຮ	Т	A	120
361	GCT	AAA	TAC	GAT	GAT	'CCA	GTT	'AAA'	.CTA	GTT	'AAA	ATG	TGG	GAA	GAI	GAA	GTG	AAA	GAT	TAT	420
121	A	ĸ	Y	D	D	P	v	ĸ	L	v	ĸ	M	W	E	D	E	v	K	D	Y	140
421	TAA	ССТ	AAG	AAA	AAG	Դ	ሞርር	GU)	חממ	ርእሮ	ilalalı I	ירייני	222	አ <i>ሶ</i> ሮ	aac	ኮልጥ	<b>'</b> ሞልር	'ል <i>ር</i> "ፐ	CAA	ልጥር፣	480
	N													T			Y			М	160
		-	•		•	-	Ū		Δ,		•	_	•	•	J	**	•	•	v		100
481	GTT	TGG	GCT.	AAC	ACC	AAG	GAA	GTT	GGT	TGT	GGA	AGT	ATA	AAA	TAC	ATI	CAA	GAG	AAA	TGG	540
161	v	W	A	N	T	K	E	V	G	C	G	S	I	K	Y	I	Q	E	ĸ	W	180
541	CAC	AAA	CAT	TAC	CTT	GTA	TGT.	AAT	TAT	GGA	ccc	AGC	GGA	AAC	TTT	'AAG	AAT	GAG	gaa	CTT	600
181	H	ĸ	H	Y	L	v	C	N	Y	G	P	S	G	N	F	ĸ	N	E	E	L	200
601	TAT	CAA	ACA	AAG	TAA																612
201	Y	Q	T	K	st	op															204



Effect of point mutations in dominating IgE epitopes hypothetical model with 3 epitopes



# **DNA SEQUENCE**

Der p 2 (DNA sequence referred to in notes in accession No. P49278 SWISSPROT)

### **ORIGIN**

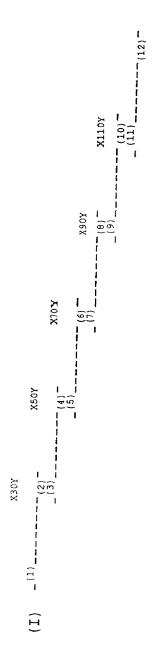
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61	cattcaaaat gatgtacaaa attttgtgtc tttcattgtt ggtcgcagcc gttgctcgtg
121	atcaagtcga tgtcaaagat tgtgccaatc atgaaatcaa aaaagttttg gtaccaggat
181	gccatggttc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccgttt
241	togaagocaa ccaaaacaca aaaacggota aaattgaaat caaagoctca atcgatggtt
301	tagaagttga tgttcccggt atcgatccaa atgcatgcca ttacatgaaa tgcccattgg
361	ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaaat
421	ctgaaaatgt tgtcgtcact gttaaagtta tgggtgatga tggtgttttg gcctgtgcta
481	ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa tttattgatt ttgtaatcac
541	aaatgattga ttttctttcc aaaaaaaaaa taaataaaat tttgggaatt c

## AMINO ACID SEQUENCE

Der p 2 (Accession No. P49278 SWISSPROT; includes signal peptide 1-17)

- 1 mmykilclsl Ivaavardqv dvkdcanhei kkvlvpgchg sepciihrgk pfqleavfea nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen vvvtvkvmgd dgvlacaiat hakird 61
- 121

Figure 17



(II) -(1)-----X30Y-----X50Y-----X70Y----X90Y----XI10Y----(12)-

Lines represents DNA sequences.

Numbers in parentheses above lines represents sense oligonucleotide primers: (1), (3), (5), (7), (9), (11).

Numbers in parentheses below lines represents anti-sense oligonucleotide primers: (2), (4), (6), (8), (10), (12).

Notation X (position) Y represents mutations.

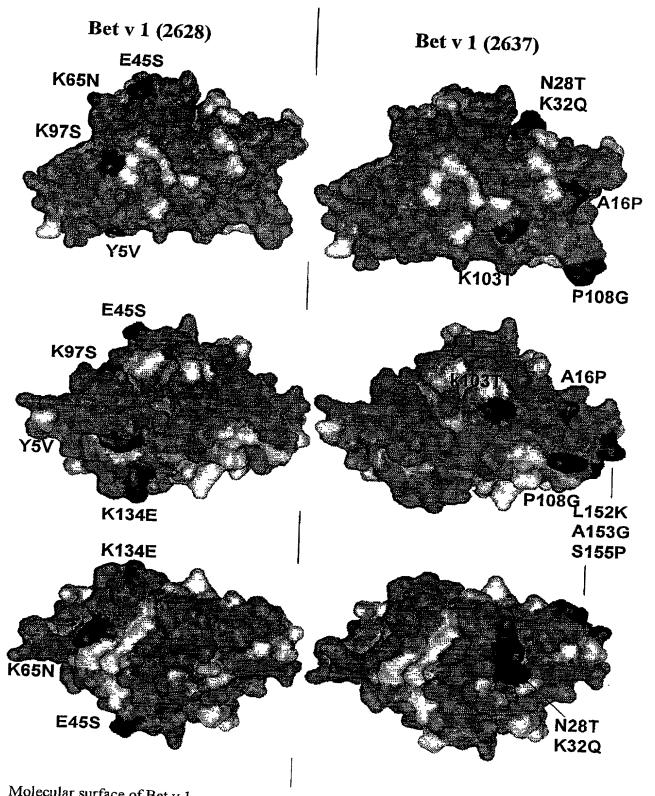
(1) Represents the sense oligonucleotide primer accommodating the protein N-terminus. (12) Represents the anti-sense oligonucleotide primer accommodating the protein C-terminus.

# 

(A16P, N28T, K32Q, K103T, P108G, L152K, A153G, S155P) DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations. 372BVa CAGACTAATTCGACGTCGGTACCC CAGTCGcggTGCTGGGATAACAGA CCAGCAccGCGACTGTTCAAGGCC CACTATGGTTATCTCGTTGGAGAT GAGATAaccATAGTGGCAACtggT 370BVa 369BVs 368BVa 367BVs Bet v 1 (2637) 331pMalc 331 pMalc 368BVa 367BVs 370BVa 369BVs Bet v 1 (2628) (Y5V, E45S, K65N, K97S, K134E) 366BV (a) 365BV (s) DNA template: Bet v 1 (2589) carrying the Y5V mutation. 364BV (a) 363BV (s) 362BV (a) 361BV (s) 189BV (a) 188BV (s) Figure 18 331pMalc (s)

CAGACTAATTCGAGCTCGGTACCC CACGTAGTTGAAAGGGAGGCCTTC GGAGATGCTCTCCAATGTGTCGCC GGAGAGCATCTCCAACGAGATAAA ACTTGCTTCAACCTGCTCTGCCTT CAGGTTGAAGCAAGTAAAGAAATG TTTCAACTACGTGAAGGACAGAGT GCAGGTCGACTCTAGAGGATCCAT AACATTTCAGGAAATGGAGGGCC TITCCIGAAAIGITITCAACACT o Ö 331pMal 332pMal 362Bva 366Bva 361BVs 364Bva 363BVs 365BVs 188BV 189BV

372BVa:TTACTGAATTCATTAGTTGTAGGCATCcggGTGgcctttGAGGTA

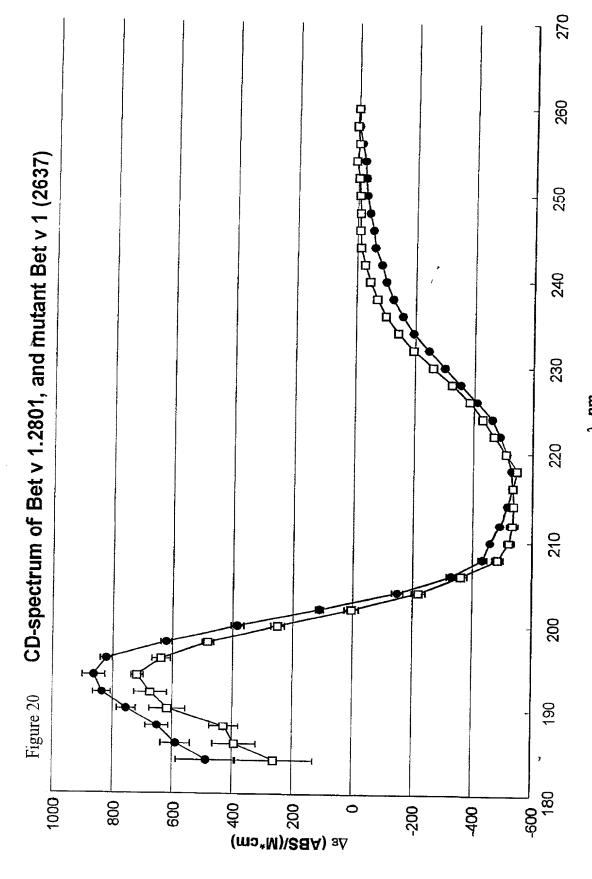


Molecular surface of Bet v 1.

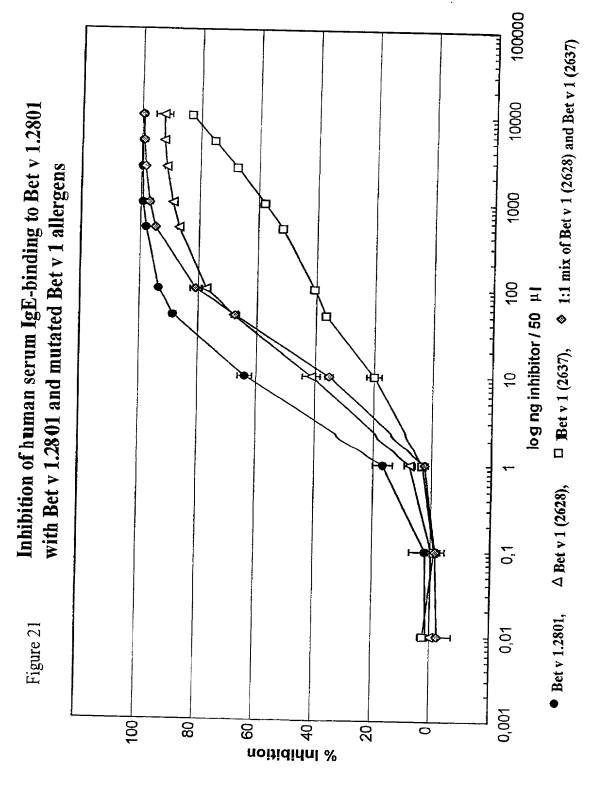
Left side: Bet v 1 (2628), Right side: Bet v 1 (2637)

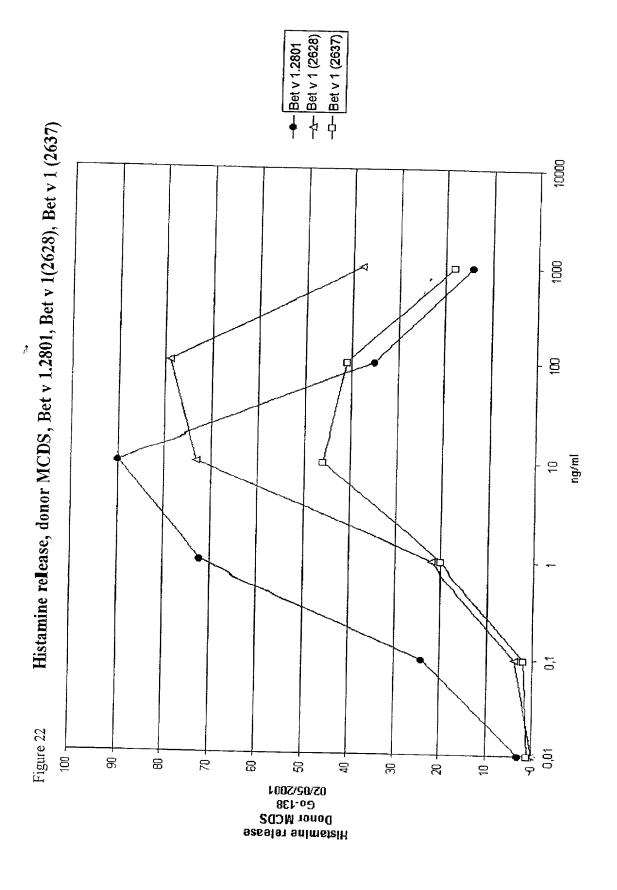
Grey: Backbone + amino acids 95-100% conserved among Fagales Black: Introduced point mutations.

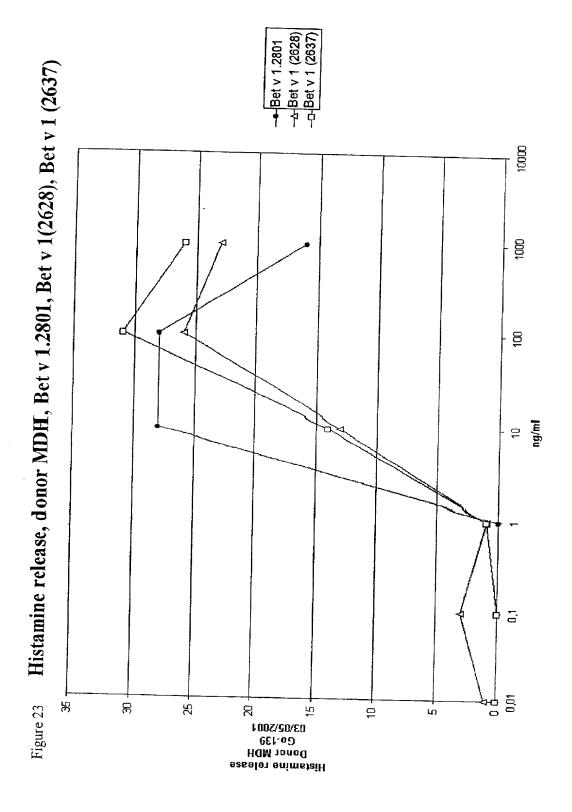
Figure 19

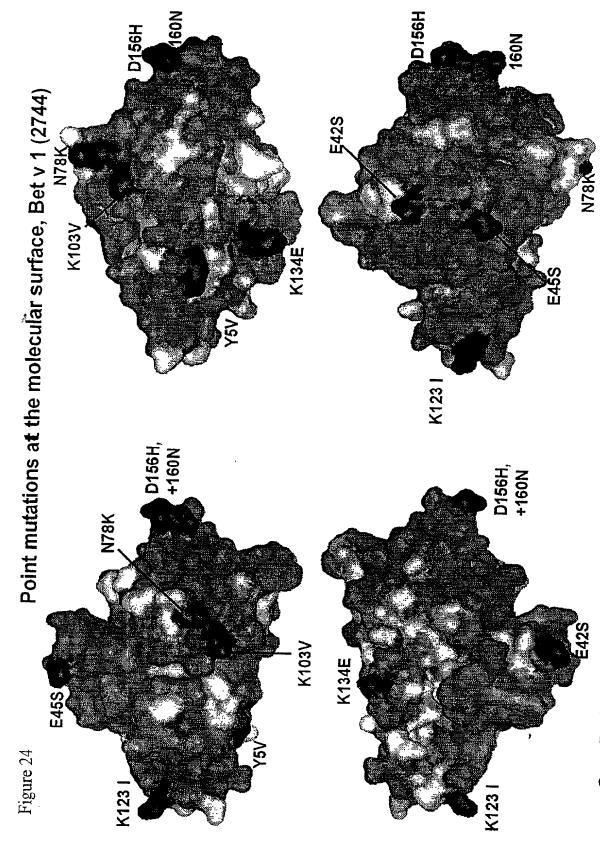


λ**, nm** CD-spectrum of Bet v 1 (2637), open squares, and the CD-spectrum of native folded Bet v 1.2801, closed circles, both obtained at 20 °C

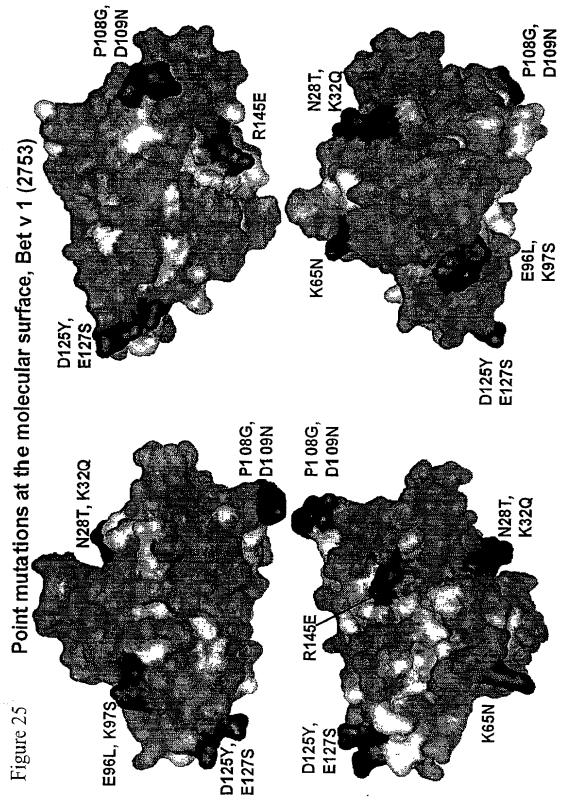








Grey: Back bone + Amino acid residues 95-100% conserved among Fagales, Black: Point mutations



Black: Point mutations Grey: Back bone + Amino acid residues 95-100% conserved among Fagales,

Distribution of point mutations at the molecular surface of, Bet v.4 (2744) [white], and Bet v 1 (2753) [Black]

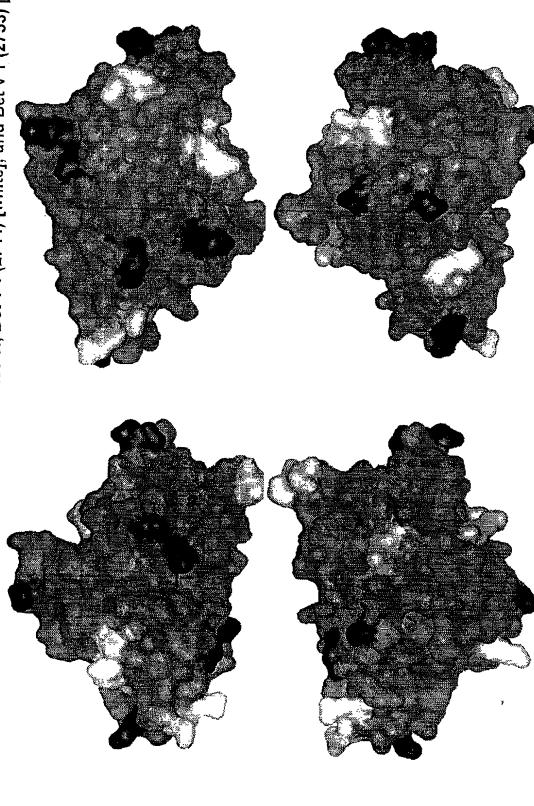
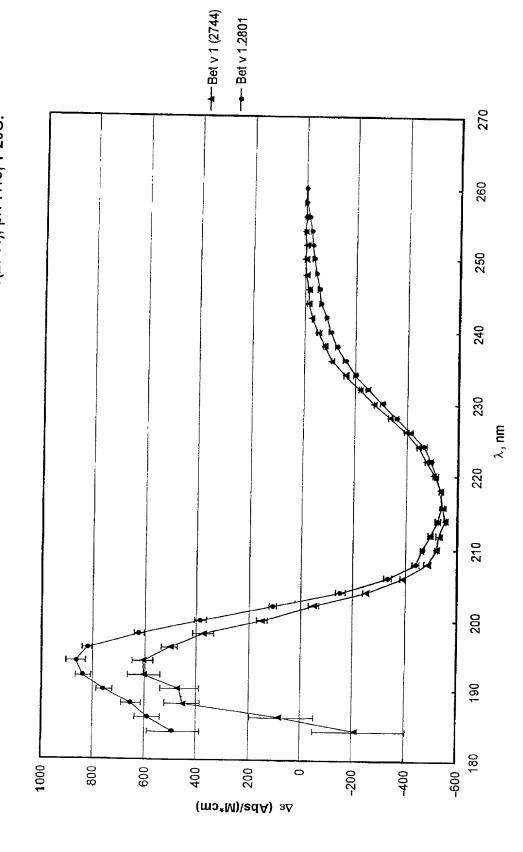
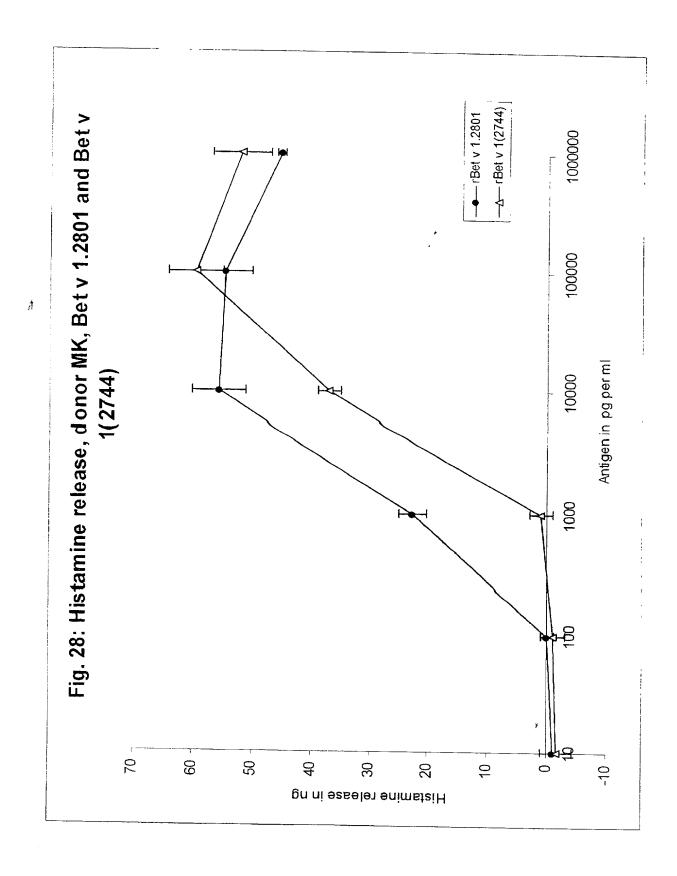
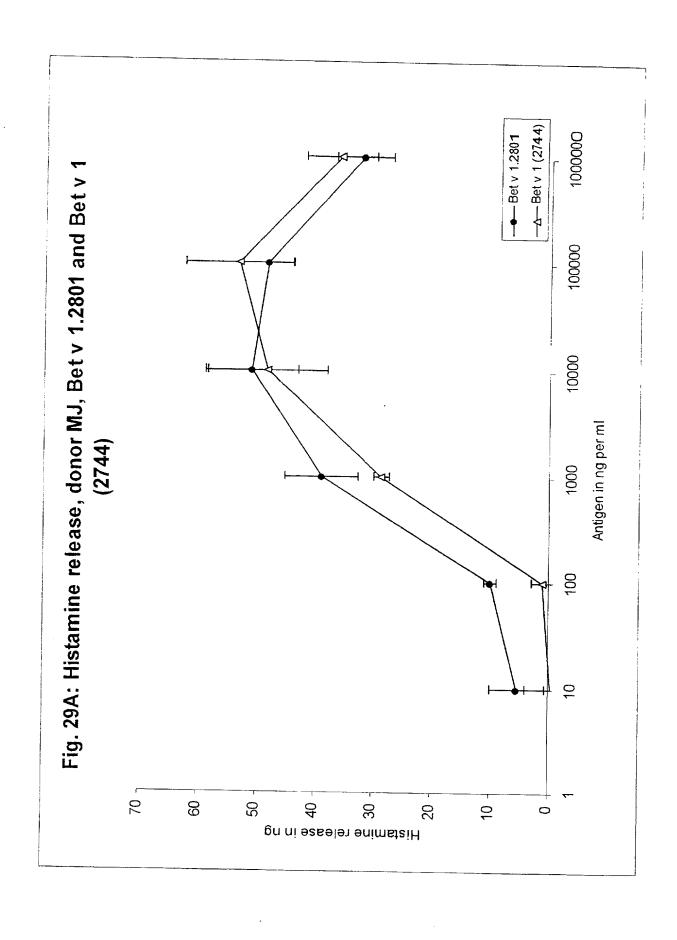


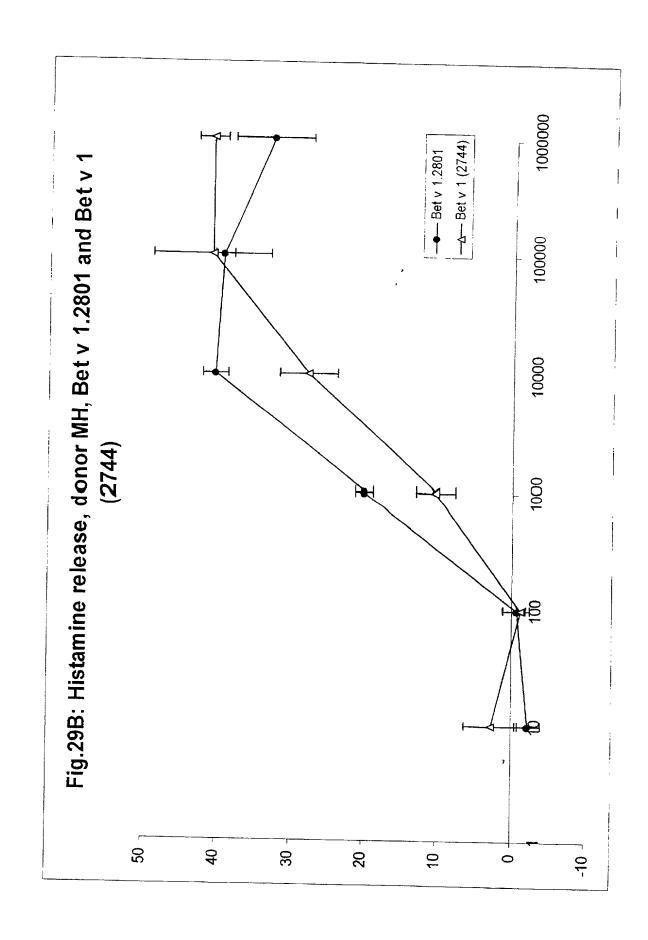
Figure 26 Grey: Molecular surface; amino acid residues 95-100% conserved among Fagales Black: Mutations (Y5V, K134E), (E42S, E45S), (N78K, K103V), K123 I, (D156H, +160N) White: Mutations (N28T, K32Q), K65N, (E96L, K97S), (P108G, D109N), (D125Y, E127S), R145E

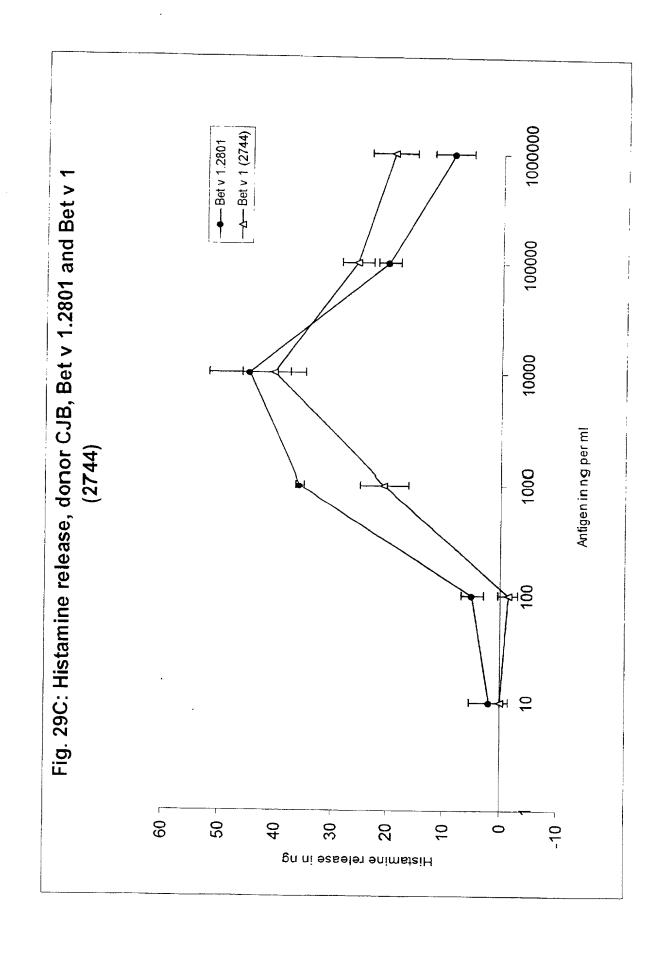
Figure 27 Circular dichroisme spectra of Bet v 1.2801 and mutant Bet v 1(2744), pH 7.13, T 20C.



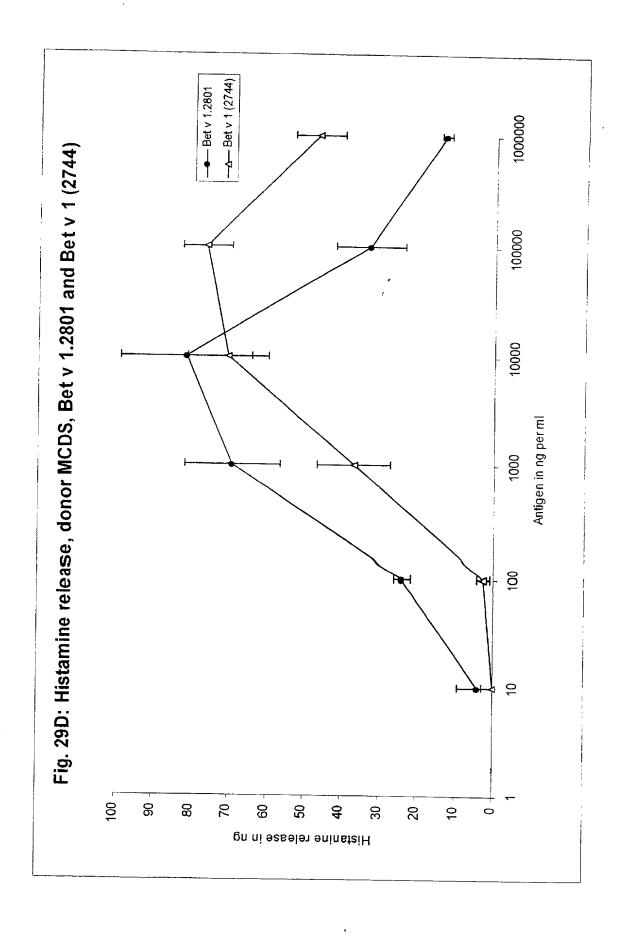


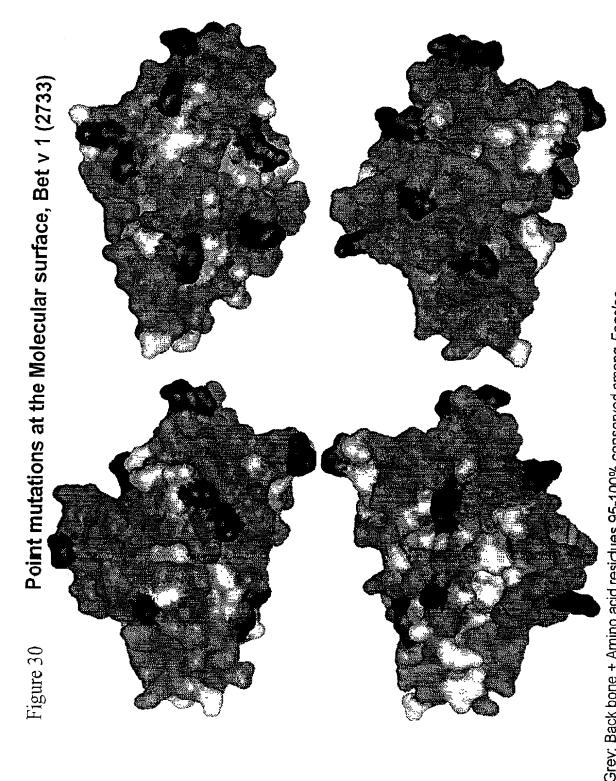






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Grey: Back bone + Amino acid residues 95-100% conserved among Fagales, Black: Point mutations: Y5V, N28T, K32Q, E45S, K65N, N78K, K97S, K103V, P108G, K134E, R145E, D156H, +160N

Figure 31

# Oligonucleotide primers for site-directed mutagenesis of Der p 2

	<b>K</b> 6∧	sense	OB43	42-mer	Xho I 5' -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
		anti-sense	OB28	39-mer	X60 I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
	K15E	sense	ОВ44	67-mer	3° -CCG <u>CTCGAG</u> AAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTTGG- 3°
		anti-sense	OB28	39-тег	Xba1 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
ş**	H30N	sense	OB46	54-mer	Epn I 5' -CGG <u>GGTACC</u> AGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC-3'
		anti-sense	OB28	39-mer	Xbo I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
	E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC-3'
		anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC-3'
	H74N	sense	OB49	32-mer	Sph I 5' -CATG <u>GCATGC</u> AATTACATGAAATGCCCATTGG- 3'
		anti-sense	OB28	39-mer	5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'
	K82N	sense	OB50	50-mer	Sph 1 5'-CTAC <u>GCATGC</u> CATTACATGAAATGCCCATTGGTTAATGGACAA CAATATG-3'
		anti-sensc	OB28	39-mer	Xba I 5' -CGT <u>TCTAGA</u> CTATTAATCGCGGATTTTAGCATGAGTTGC-3'

3.0			
2 0		PG 1 0 P R A C	
10			
-	A A V V A D D O O O O O O O O O O O O O O O O O		
. 1 0	N		
	PDB 000855 000855 000855 000855 000855 000855 0008520	H G K P P P P P P P P P P P P P P P P P P	PDB
	1 DERPZ-ALK-G Der p 2 2 DERP 2 CDNA Der p 2 3 DERPZ-ISO101 Der p 2 4 DERPZ-ISO102 Der p 2 5 DERPZ-ISO103 Der p 2 5 DERPZ-ISO103 Der p 2 7 DERPZ-ISO103 Der p 2 8 1 A9V 9 DEF 2 DERFA Der (2 10 B61241 Der (2 11 AHK Der (2 12 A61501 Der (2 13 -09630 Eurm 20102 14 Q97222 Eurm 20102	1 DERPZ-ALK-G Der p 2 2 DERP Z CDNA Der p 2 3 (DERPZ-ISO101 Der p 2 4 DERPZ-ISO102 Der p 2 5 (DERPZ-ISO102 Der p 2 6 (DERPZ-ISO103 Der p 2 7 DERPZ-ISO103 Der p 2 8 148V 9 (DER PZ-ISO103 Der p 2 9 (DEF 2 DERF A Der f 2 11 1AHK 11 1AHK 12 AG1601 13 (OSG430 Eur m 20101 14 OSTZZ Eur m 20102	1 DERP2-ALK-G Der p 2 2 DERP2 CDNA Der p 2 3 DERP2-ISO101 Der p 2 4 DERP2-ISO102 Der p 2 5 DERP2-ISO103 Der p 2 6 DERP2-ISO104 Der p 2 7 DERP2-ISO104 Der p 2 8 1.69V 9 DER 2 DERFA Der f 2 10 661241 Der f 2 11 1.4HK Der f 2 13 096430 Eur m 2 01012 091722 14 091722 Eur m 2 0102 091727

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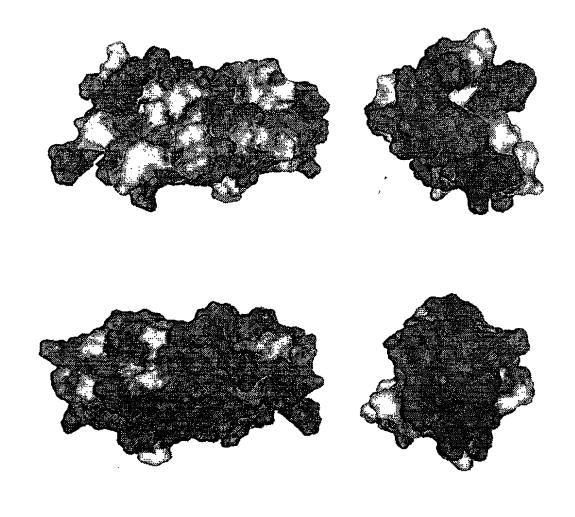


FIG. 33: Der p 2

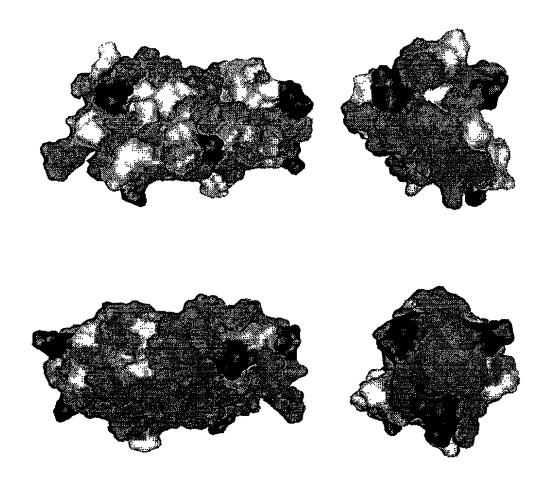


FIG. 34: Der p 2 mutant

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7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7	1	
1 2 0 1 2 0	4 8 0 8 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
1	1.7 0 1.7 0 1.0 0	
100 100 100 100 100 100 100 100		2 2 0 2 2 0 2 2 0 2 2 0 3 5 7 7 7 8 6 3 5 6 7 7 7 8 6 3 6 7 7 7 8 6 3 6 7 7 7 7 8 6 3 6 7 7 7 7 8 6 3 7 7 7 7 8 7 7 8 7 7 8 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 7 8 7 8 7 7 8
		2.10 2.10 3.5 F A A B B B B B B B B B B B B B B B B B
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1.4.0 1.	1.0
Der p1 AUK spiPOB178 MMAL_DERPT_Der p1 AUK info@UGA0 GEUBA0 Eur m1 0101 auf GBTZZ3 GSTZZ3 Eur m1 0102 spiPOB31 MMAL_DERFR Der f1 spiPOB31 MMAL_DERFR Der f1 info@GSZQ4AGGGSZ0 Der f1	Der pl ALK spiPOBITGINAAL_DERPT Der pl tradelle bernation of trade	Der p1 ALK seiPOBITBINNAL_DERPT Der p1 InfoBUBAGIGSUBAD Eurm 1 0101 InfoBITZATOSTITZA Eurm 1 0101 InfoBITZATOSTIZZA Eurm 1 0101 SPIP 1631 III MAAL, DERFA Der f1 SPIP 257 160 EURMA EURMA Eurm 1 InfAAGOOSZOJAAGOOSZO Der f1

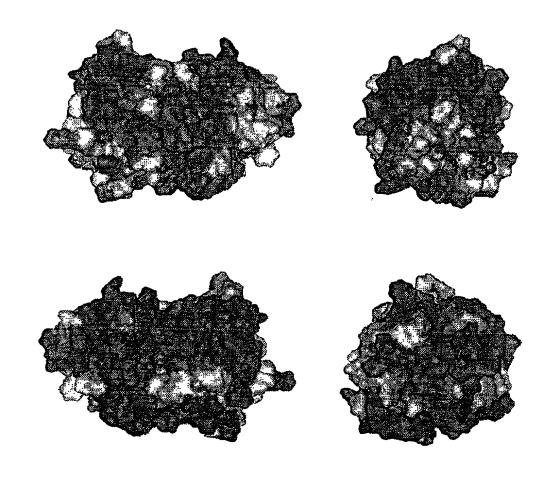


FIG. 36: Der p 1

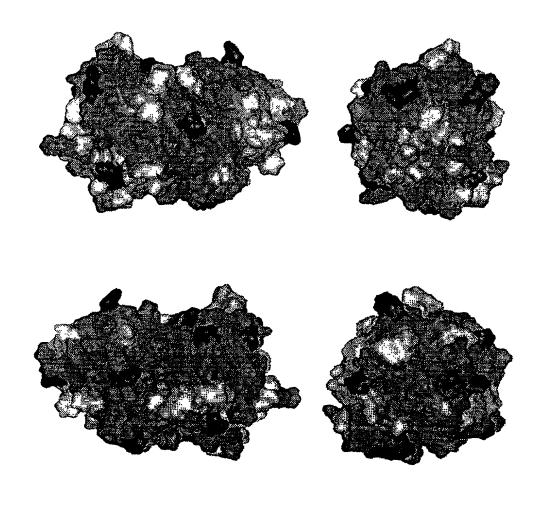


FIG. 37: Der p 1 mutant

FIG. 38A (Phl p 5)

110.0011	111 p 0)				. , .		;						
i	:			2 0		!	¿ ·	3 0	•		;		
tr 081341 081341	PH p 5.0103	·····	- , - M·A	VHQY	4		LAV	À L V	:-		,	٠.,	
triQ40960 Q40960 epiQ40962IMPSA_PHLPR	Phip5	- · · · · · · · · · · · · · · · · · · ·	- M A	A H O A	TYA	L F	L.A.V.	A L V	· p.:		1111111	11, 171.	٠.
spiP22206 MP92_POAPR	Poe p 5 (KBG41)	· ; - ; -	A.M.	VHQY			L A V	ALV		,-,		Tirturia Tirturia	: :
spiP22286[MP93_POAPR triQ65319(065319	Pos p 5 (KBG60) Phi p 5	` -;	- ;;• , Ķ, Ā	Y Q K Y	TYA	<u>.</u> L.F.;	ŗ., v.	AŞL VI	- , - i -	• • • • • • • • • • • • • • • • • • • •	• • • • • • • •		• •
triO65320 O65320	PH p 5		ing American Section (1997).								7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7	·: · : · ·	<u> </u>
tr 065321 065321	Phip 6									. [. j. j	-14	·	
trj066318(066318 trjP93467(P93467	PH p 6 PH p 5				H-1:1:			312 34.	: : : : : : : : : : : : : : : : : : : :	:	:-: <del> </del> - - -		٠,٠
spiP22284IMP91_POAPR	Poa p 5 (KBG 31)		M D K A	HGAY	KTA	LK	A A S	וֵ <sup>י</sup> ֹם עַוֹּמְ	A E	K F P	V E O A T	FDKN	LK
spiQ40237IMPSB_LOLPR triQ9XF24 Q9XF24	Lol p 58 Lol p 5A	4.5.1		VQKH				A, L V . A: L V .	• • •	:	• • • • • •		
140320331032038	Lot p 5C			VOKY				À L V		* *			•
1/10813431081343	Phl p 5 0206		·M.A.	V Q K Y	T.V.A	L.E	LAĮV	A.L.V		٠.	*		
tri023972 023972 tri081344 081344	Holl5 Phlp 5 0207		. MA	V Q K Y	TVA	LiF	LAV	A.L V	-				
tn[AAG42255]AAG42255	Holi5B		M A	V Q K Y	T V A	L EÎ	ĹŢŢ,	A L V	. , . , .				
In/AAG42254/AAG42254 In/OB1342/OB1342	Poa p 5 Phi p 5 0203	SVK			T V A		LTV PRR	ALV.	;-	;		• • • • •	• -
tr/P93466/P93466	Phip5					AV		G P R		-1- ::			
spiQ40963jMP58_PHLPR triQ9S8E0jQ9S8E0	PN p 58 PN p 5.0204				AAA	AV	P'R R	G P R					· :
tdO239711O23971	Phi p 5.02								: r.				
EPIPSG166IMPS3_PHAAQ HAAQ	Phe a 5.3 Phe a 5.1		M A	V Q K Y	TVA	C F	LAW	AL V	Ja[±:				- , <i>-</i>
1/10048281004828	Horv9		MANS	GREH	AMT	L F	RRN	LVA				• • • • • • • • • • • • • • • • • • • •	
tr Q39995 Q39996	Hory 6 (30kDa)		إعرابات		<u> - - </u> -		: ( <u>-</u>	· · · · ·	· ; - ,	:	٠, إ٠ -٠٠,	, . ,	
}							····		-h :			4-	- 4
1			10		<b> </b>	2					3 0		•
trj061341j081341	PN p 5.0103		. Intriis	ATA PIK	micir	arvinesi	i in an	cia en			. MED	A CONTACT	<b>4</b> .
triQ40960jQ40960	Phl p 5								Ε	- [ - ] - [	- A A		
sp Q40962 MP5A_PHLPR sp P22265 MP92_POAPR		PAT		A THE	PIA	AG				:+::+:	DA		
spiP22296IMP93_POAPR	Pos p 5 (KBG60)	P		A T ESA	APA	AG	7 100	V. V.	<b>.</b>		- A A	k.,	
1/1065319/065319 1/1065320/065320	Phip5					G B			# E - :	탁투다	<b>M</b> AR		<b>.</b>
110653211065321	Phi p 5					G	Y Y		E -		AAD		
14065318)065318	Phi p 5					e n		0.00	E .		- · A A	A G A A	-
tr P90467 P93467 sp P22284 MP91_POAPR	Phip 5 Posp 5 (KBG 31)	РРА	S.K.F	A K MA	PKV	A A	7		6	• ; • • • • •	A A	KA	10 - 10
6PIQ40237 MP5B_LOLPR	[Lol o 58]	T.A	PATP	A A P A	TAA		4 J P.,	N T P /	T P		AAV		<b>8</b> -
triQ9XF24 Q9XF24 triQ9SC99 Q9SC99	Lolp 5A Lolp 5C	- SERE	; :. •				AA	TP	T P	ΑΑ 1 ΑΑ 1	PAAAG	GGKA	
triO81343jO81343	Ph 5 0206		Try Try	74		A		W . P		- · · · · · · · ·	. A.E.	KGKA	ğ.
tri023972 023972 tri081344 081344	Hol ( 5 Phl p 5.0207						A		<b>.</b>			GIGINA	
tn/AAG42255/AAG42255	Hol I 58					Ā				1-:1	AA	A CHIL	P
tnjAAG42254jAAG42254 (rlO81342)O81342	Po# p 5 Phi p 5.0203		::	: : : : : : : :		A B		<b>**</b>		4-1:1:	A .	A CONTRACT	P
tr/P93466/P33466	PN p 5					Â							
epi040963 MP6B_PHLPR						A		<b>₩</b>	<b></b>		A		<b>.</b>
triQ9SBE0/Q9SBE0 triQ23971/023971	Phi p 5.0204 Phi p 5.02		11111	:   -   -   -		A MONTH	X 100 00 X 400		Name of the last		<b>120</b> -200-2	96331,0823623	<b>6</b> 8
spP56166MP63 PHAAC	Pha a 5.3				G			T M		Α	PGAA	A WELL	<b>E</b> :
HAAQ tri004828(004826	Phsa51 Horv9		· · · · · · · · · · · · · · · · · · ·	N SEELS F	PVF	N R		T			PPPR	RDK	
14039995 039995	Horv 5 (30kDa)	1.1.		*******	<u> - -;-</u>		interior		2000000		* -: ', -, -		_
		,÷i-							·····				
	,	9	oi		1	<b>0</b> 0		Ĭ., Į.	1111	0 1	, , , , , <b>, , , , , , , , , , , , , , </b>	2.0	
1/10813411081341	PN p 5.0103					X III						a Trice	N. Ke
1/0409601040960	Phi p 5	ESTA	1				100	0.0		(1) Y	STATES	a rat E	
spiO40962IMP5A_PHLPR spiP22286IMP92_POAPR		-		A A	<b>13</b>								
spiP22286 MP93_POAPR	Pos p 5 (KBG60) :			A V O S			15.00				SALG	2 T P E	
tri0653191065319 tri065320[065320	Phip5	THE ST	<b>A</b>	A L S S	S. K. A	<b>A</b>			* 1	7.1	( T A 1 G ( T A 1 G	A TOPE	
1/10653211065321	Phip5	2017/1999/2005/5/20	7/2	A E S 9	V 8 A	A	6.				CITALE G	AT PE	<b>X</b>
1/1065318 065318	Phip5	E # 8 4 E # 8 4			S 3 A	A L	2.6	D A		L A Y	STALE G STSEG	ATPE/ ATPE	E
sp(P22284)MP91_POAPR	Phi p 5 (KBG 31)	E P K		ATES	S & G S & A	V L	5 1	E A I	Y K	AY			
sp(Q40237)MP5B_LOLPR	Lol p 58	1	5 - Y	D Q	265-3868 N	Q W	S ( )	DA	L	. A Y I	AAQG	ATPE	<b>4</b>
triQ9XF24 Q9XF24 triQ9SC99 Q9SC99	Lol p 5A Lol p 5C	. 1.1.1.		A K A P		G	L	D 7 0	D '	V A V	AGE	ATPE	A K
trj081343j081343	`Phlip50206`			- A P		G V	V P	9 4 2	S S	V A V		ATEC	N.
14023972 023972 14081344 081344	Hall 5 Phl p 5 0207	,	💥	T K A P -:-;A P		G				T AND A	AAAQG	A T P E	
1nJAAG42256JAAG42255	Hol 158			QAP		G F				A T	A D VIS		
1nAAG42254\AAG42254	Poa p 5			QAP	1 - 1 - 1	G:F	V B H N	V A A	SD	A T Y	53 A 3563 V 6623		
trj081342j081342 trjP93466jP93466	;PH p 5 0203 ;PH p 5			A P		Ğ	V P V P	A F	5		AAV	AT FE	
epiQ40963IMP5B_PHLPR	PH p 58			. A P		G	V P K		2 2	y A		ar es.	X
1/JQ9SBE0 Q9SBE0 1/JQ23971 Q23971	PN p 5.0204 PN p 5.02		i i i i i i i i i i i i i i i i i i i	ETKM	p :	G L		漢V D製	M M	A A F	ASTG		K
spiP56166[MP53_PHAAQ	Pha e 5.3	. , . ,		STKG		1	-:-:- <b>3</b>		S	v veri	Y Y A A ST	ATPE	
HAAO HOO4828 004828	Pha a 5.1 Hor v 9	AATE	o i	T K A	M M	C E	K A K		R	V IX Y I		STORE	
11/039995 039995	Hor v 5 (30kDá)		Market Mark		1985)			EL			KROO	ATTHE	
				•	<b>†</b>	. 1				, , .			

FIG. 38B (Phl p 5)

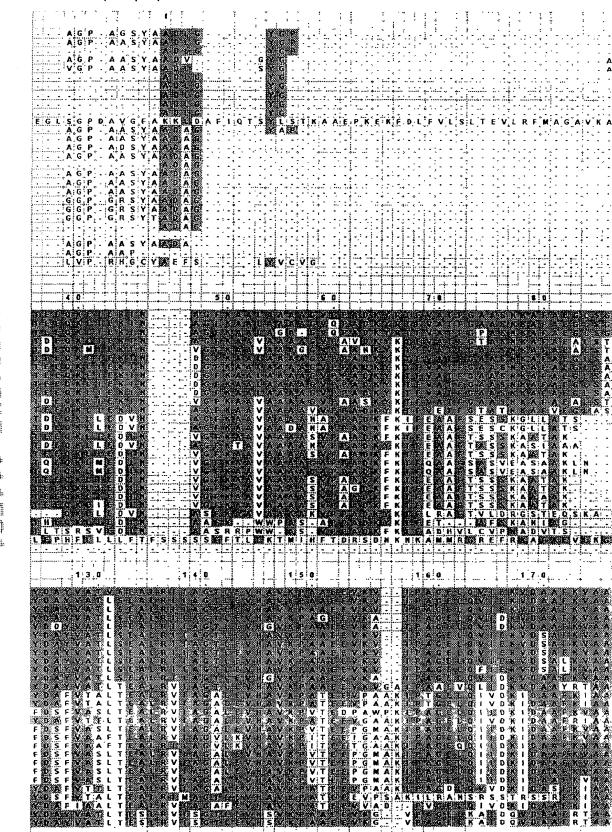
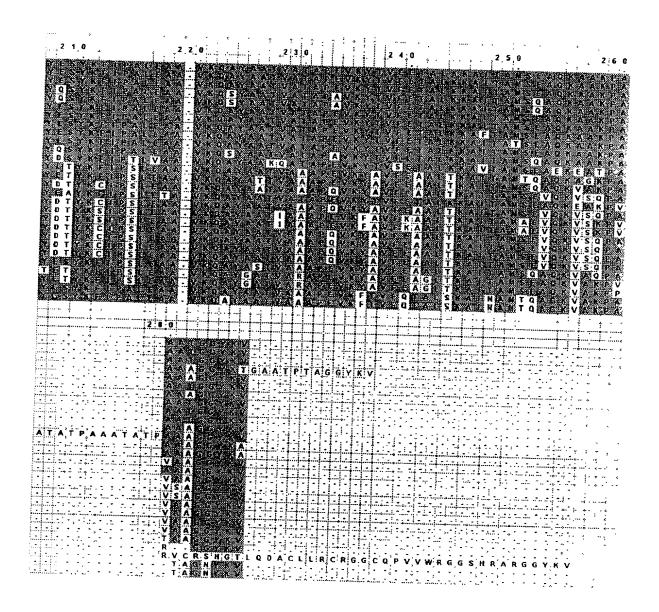


FIG. 38C (Phl p 5)

*******					i i		1
Sancia	*		+	1 8 0	1 9	io	2 0 0
triO813411061341	Pht p 5.0103	1	* † . , † .				
tr Q40960 Q40960	PN p 5	4					
spiQ40962MP5A_PHLPR	PN p 5 A		*****				F
sp[P22285[MP92_POAPR		, 7 . <b>*</b>		THE R H AVE L	SMAN REPORT OF THE		DECEMBER OF STREET
*pIP22286 MP93_POAPR				real at the syl	2 (2 110) (5 (20)		DA ERASTIC CA
tr O65319 O65319	Phi p 5			Tig and start	and the second	OF EAR FEEL	NAME KEASSING IT A
tr 065320 065320	Phips	:-	•, • , •   •				HALLKAST G G A
tr 066321(066321 tr 066318(066318	Phip5 Phip5		r acrosytyty				NATE ASTEGA
(dP93467)P93467	Phi p 5						M A S A S A S A S A S A S A S A S A S A
spIP22284 MP91 POAPR	Pos p 5 (KBG 31)						
spiG40237jMP58_LOLPR						VER NITE N	NA LKVS LEADA
InQ9XF24 Q9XF24	Lolp 5A			TALA NIA ALI	TNORES	WEE SINE N	XALKECTESA
14092C99109SC99	Lot p SC		<u>  -                               </u>	* A 11 (A) A 1	TROWEST	NAME & S ASSESSME	KALKECIEGA
tr 081343 061343 tr 023972 023972	Phl p 5 0206			AATA	A D DESCRIPTION		KATKESTEGGA
tr 081344 061344	Hol 15 PN p 5 0207				VINCER	Gr. v	KALEKESUEGA
tn/AAG42255/AAG42255	Hol 15B			AAH	A D		
tn/AAG42254/AAG42254	Pos p 5						
tr(081342 061342	PM p 5 0203	1		TA A A TIA	A D owner		K MANUFACTURE AND A SECOND
Ir(P93466(P93466	PN p5			TAXA A TAXA	D Carrier		KANDEKEKEEGA
splO40963(MP6B_PHLPR	Phl p 5B			A A A A	Door		KANDA EKILEGA
tr(Q9S8E0(Q9S8E0	Phl p 5.0204			AIT		10.00	K PENNEK E STAFFE A
tr(023971 023971 apiP561661MP53 PHAAQ	Phi p 5.02 Pha e 5.3	TVÄ		5			KALKEKAGEA
HAAG	Pha # 5 1	* * * * * * * * * * * * * * * * * * *	PLSHS	\$ 1		G G	KA KERHEGP
ft/004828 004828	Hory 9			CHARLED BALLET			
tr(039995 039995	Hor v 5 (30kOs)		. 7 - 1 - 1 - 1 - 1 - 1	CARLA D ALAS	rajen eg g	22020002410228	GPSRKPRK GA
to the second							
	,		: 4.1.4	.	<u> </u>		
				1 1 1 1 1 1 2	7 0		
triO813411O81341	PN p 5 0103	7 1000	*		THE WATER CONTRACT OF THE PARTY.	mer : 1	
tr Q40960 Q40960	Phi p 5			A SECOND AND			GALAN
spiQ40962IMP6A_PHLPR	Phi p 5 A	<b>A.</b>		- KARIBANIANI	20 0 M C 20 1		GAAL
spiP22265[MP92_POAPR	Pos p 5 (KBG41)		. (-)-1-1-1-1-1	· W T (A, T A T	GAVGAR	GA V GAA	TG A AT
spiP22286(MP93_POAPR 11/065319/065319	Poa p 5 (KBG60) Phi p 5	T E		A I G I A I		<b>*</b>	· G A A T
tdO65320(O65320	Phip 5	N.A.			5 4 4 5 4 4		GA THE
triO653211O65321	Phi p 5	TE					
tr 065318 065318	Phip5	T : E		A TEATERS	A A V. C. A S		- G A A I
tr P93467 P93467	Phi p 5	T'E		- JA 180 - 191			IGAATI.
spiP22284[MP91_POAPR spiO40237[MP5B_LOUPR	Pos p 5 (KBG 31)		لله بدر والمسلس	V I G A	SANGA		- G-6-6-10-1
triQ9XF24IQ9XF24	85 م اما 58 م اما			A THAT PR	PAAATA	A PAAA	Y A TEAT P A A A T
(dGBSC39)Q9SC99	Lolp 6C				<b>V</b> a†kaa	A THE STATE OF THE	AR GIAT
tri081343 081343	Phi p 5.0206	T G		ANVAAG		G A.A	S E X A.T
tr 023972 023972	Hol 15			NT - G:	A A T A A	G V A	AGAAT
tr 081344 061344	Phi p 5 0207	T G		AAAAG		G A A	SSAAT
InJAAG42255JAAG42256 InJAAG42254JAAG42254	Hol 158	G A A	12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	AATG	ASSA I GREEN	G A A	[ <b>5 A A 1</b> ]
tr(081342)081342	Pos p 5 PN p 5.0203	TG	LI VIA A	A C V A L G			
tr(P93466)P93466	PN p 5	TG		AND VARO		G A A	
	PN p 58	T G		VALG		G A A	S ICON IN THE STATE OF THE STAT
tr(09SBE0 Q9SBE0	PM p 5.0204	T G		ARTVALG	AN TITE	G A A	S IS SO SO TO .
tdO23971(023971	Ph 1 p 5 02	. A .		N - 4 = 1 - 4 - 4 - 1 - 1	T 8	1 V A	A MUTA A TE
	Phas 53	R L S P		PPOVILPL	, c	V.A	Alaisid S
tri0048281004B28	Pha a 5,1 Hor v 9	L S P		PPQVLPL	A C C C C	×	A,A:S;D.V -,
triQ39996[Q39995	Hor v 5 (30kDa)	-14.2		14 4 12 4 1	V X A S X X		
		////		XTACOOR PLANTED TO THE ACTION AND ACTION			

FIG. 38D (Phl p 5)



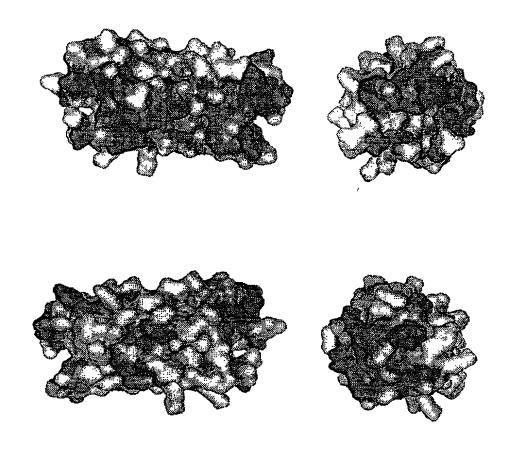


FIG. 39A: Phl p 5, Model A

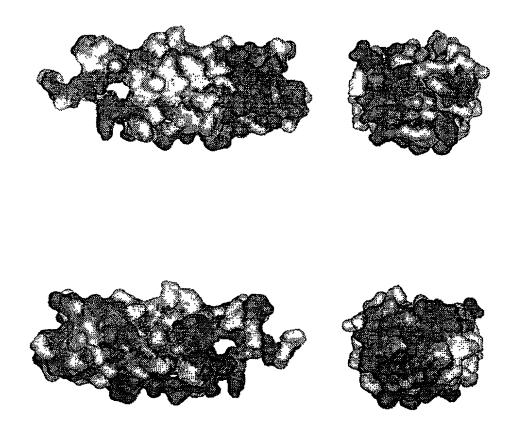


FIG. 39B: Phl p 5, Model B

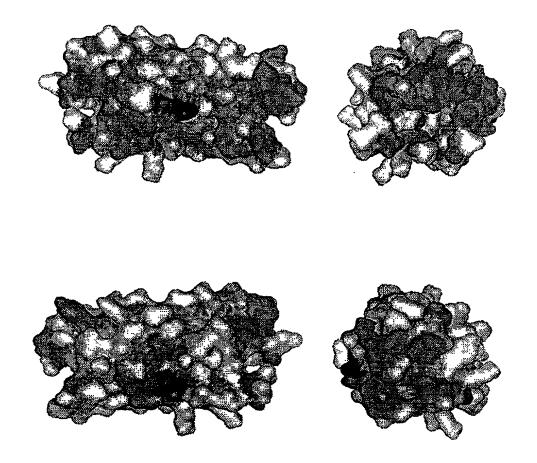


FIG. 40A: Phl p 5 mutant, Model A

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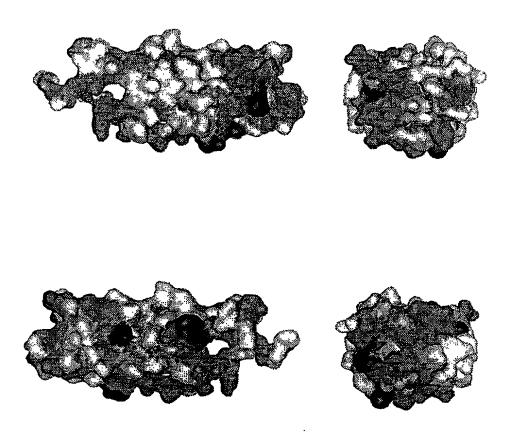
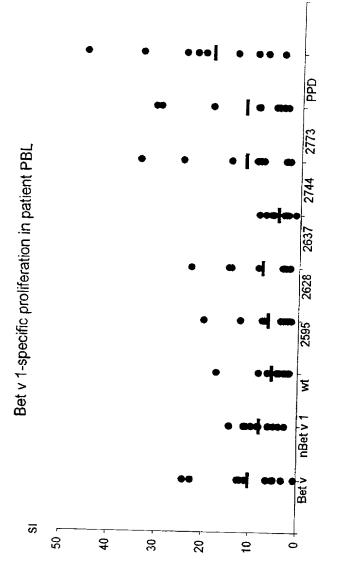
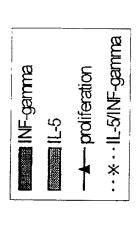


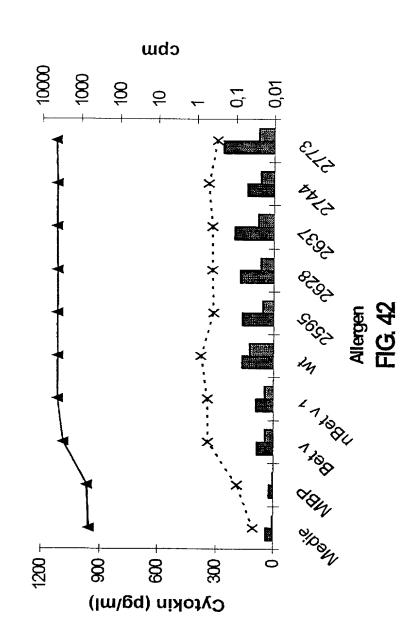
FIG. 40B: Phl p 5 mutant, Model B

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samples Figure 41: Stimulation of Bet v 1





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